

ABSTRACT

[0117] Method for the identification of genes and genetic signals based on the structural properties of DNA double-helix comprising the following steps:

[0118] A - using the classical physical model of helix-coil transitions,

[0119] B - calculating stability curves (probabilities of opening of the DNA double-helix, along a given sequence) by algorithmic methods),

[0120] C - determining the disruption in the linear DNA for different temperatures,

[0121] D - analysing the stability curves for the detection of genetic signals (disruption of the double-helix) or the identification of coding regions (simple genes or exons in split genes as regions of high thermal stability), and optionally,

[0122] E - based on the structural informations, performing classical sequence analysis (donor/acceptor sites, start and codon stops, in correspondence with the frontiers identified in the stability curves and open reading frames analyses) for completing the identification of genes.